

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/394,020B DATE: 11/29/2000
TIME: 16:13:44

Input Set : A:\Huv3201.app
Output Set: N:\CRF3\11292000\I394020B.raw

3 <110> APPLICANT: PEPICELLI, CARMEN V.
4 LEWIS, PAULA M.
5 MCMAHON, ANDREW P.
7 <120> TITLE OF INVENTION: REGULATION OF LUNG TISSUE BY HEDGEHOG-LIKE POLYPEPTIDES,
8 AND FORMULATIONS AND USES RELATED THERETO
10 <130> FILE REFERENCE: HUV-032.01
12 <140> CURRENT APPLICATION NUMBER: 09/394,020B
13 <141> CURRENT FILING DATE: 1999-09-10
15 <150> PRIOR APPLICATION NUMBER: 60/099,952
16 <151> PRIOR FILING DATE: 1998-09-11
18 <160> NUMBER OF SEQ ID NOS: 30
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1277
24 <212> TYPE: DNA
25 <213> ORGANISM: Gallus sp.
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(1275)
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34 1 5 10 15
35 tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc 96
36 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
37 20 25 30
38 att gga aaa agg agg cac ccc aaa aag ctg acc cgg tta gec tat aag 144
39 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
40 35 40 45
41 cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga 192
42 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
43 50 55 60
44 tat gaa ggg aag atc aca aga aac tcc gag aga ttt aaa gaa cta acc 240
45 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
46 65 70 75 80
47 cca aat lac aac cct gac att att ttt aag gat gaa gag aac acg gga 288
48 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
49 85 90 95
50 qct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg 336
51 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
52 100 105 110
53 gcg atc tgc gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc 384
54 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
55 115 120 125
56 gag ggc tgg gac gag gat ggc cat cac tcc gag gaa tgg ctg cac tac 432
57 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
58 130 135 140

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72	tac	ggc	atg	ctg	gcc	cgc	ctc	gcc	gtc	gag	gcc	gcc	tcc	gac	tgg	gtc	528		
73	Tyr	Gly	Met	Leu	Ala	Arg	Leu	Ala	Val	Glw	Ala	Gly	Phe	Asp	Trp	Val			
74						165			170							175			
76	tac	tac	gag	tcc	aaq	qcg	cac	atc	cac	tgc	tcc	gtc	aaa	gca	gaa	aac	576		
77	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn			
78						180			185							190			
80	tca	gtg	gca	gca	aaa	tca	gga	ggc	tgc	tcc	cct	ggc	tca	gcc	aca	gtg	624		
81	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val			
82						195			200							205			
84	cac	ctg	gag	cat	gga	ggc	acc	aaq	ctg	gtg	aag	gac	ctg	agc	cct	ggg	672		
85	His	Leu	Glu	His	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly			
86						210			215							220			
88	gac	cgc	gtg	ctg	gtc	gtc	gct	gac	gca	ggc	ctg	ctc	tac	agt	gac	720			
89	Asp	Arg	Val	Leu	Ala	Ala	Asp	Ala	Asp	Gly	Arg	Leu	Leu	Tyr	Ser	Asp			
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92	tcc	ctc	acc	tcc	ctc	gac	cg	atg	gac	agc	tcc	cga	aag	ctc	tcc	tac	768		
93	Phe	Leu	Thr	Phe	Leu	Asp	Arg	Met	Asp	Ser	Ser	Arg	Lys	Leu	Phe	Tyr			
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96	gtc	atc	gag	acg	cg	cag	ccc	cg	gg	ctg	cta	ctg	acg	g	g	cc	816		
97	Val	Ile	Glu	Thr	Arg	Gln	Pro	Arg	Ala	Arg	Leu	Leu	Thr	Ala	Ala				
98						260			265							270			
100	cac	ctg	ctc	ttt	gtg	gcc	ccc	caq	cac	acc	cag	tgc	gag	gcc	aca	ggg	864		
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102						275			280							285			
104	tcc	acc	agt	ggc	cag	g	cc	gtc	ctc	gcc	agc	aac	gtg	aag	cct	ggc	912		
105	Ser	Thr	Ser	Gly	Gln	Ala	Leu	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Gln			
106						290			295							300			
108	cgt	gtc	tat	gtg	ctg	ggc	gag	gg	cag	cag	ctg	ctg	ccg	g	q	tct	960		
109	Arg	Val	Tyr	Val	Leu	Gly	Glu	Gly	Gly	Gln	Gln	Leu	Leu	Pro	Ala	Ser			
110	305					310			315							320			
112	gtc	cac	agc	gtc	tca	ttg	cg	g	g	gtc	tcc	gga	gcc	tac	gcc	cca	1008		
113	Val	His	Ser	Val	Ser	Leu	Arg	Glu	Glu	Ala	Ser	Gly	Ala	Tyr	Ala	Pro			
114						325			330							335			
116	ctc	acc	gcc	caq	ggc	acc	att	ctc	atc	acc	cgg	gtg	ttg	gcc	tcc	tgc	1056		
117	Leu	Thr	Ala	Gln	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys			
118						340			345							350			
120	tac	gcc	gtc	atc	gag	gag	cac	agt	tgg	gcc	cat	tgg	gcc	tcc	gca	cca	1104		
121	Tyr	Ala	Val	Ile	Glu	Glu	His	Ser	Trp	Ala	His	Trp	Ala	Phe	Ala	Pro			
122						355			360							365			
124	tcc	cgc	ttg	gtc	cag	ggg	ctg	gtg	gcc	gcc	ctc	tgc	cca	gat	ggg	gcc	1152		
125	Phe	Arg	Leu	Ala	Gln	Gly	Leu	Leu	Ala	Ala	Leu	Cys	Pro	Asp	Gly	Ala			
126						370			375							380			
128	atc	cct	act	gcc	cc	acc	acc	act	ggc	atc	cat	tgg	tac	tca	cg	g	1200		
129	Ile	Pro	Thr	Ala	Ala	Thr	Thr	Thr	Gly	Ile	His	Trp	Tyr	Ser	Arg				
130	385					390			395							400			
132	ctc	ctc	tac	cgc	atc	ggc	agc	tgg	gtg	gt	gat	gg	gt	gac	g	cg	ctg	cat	1248

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133 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
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138 420 425
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141 <211> LENGTH: 1190
142 <212> TYPE: DNA
143 <213> ORGANISM: Murine sp.
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (1)..(1188)
149 <400> SEQUENCE: 2
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152 1 5 10 15
154 gca cta tct gcc cag agc tgc ggg ccg qgc cga gga ccg gtt ggc cgg 96
155 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
156 20 25 30
158 cgg cgt tat gtg cgc aag caa ctt gtg cct ctg cta tac aag caq ttt 144
159 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
160 35 40 45
162 gtg ccc agt atg ccc gag cgg acc ctg ggc gcg agt ggg cca gcg gag 192
163 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
164 50 55 60
166 ggg agg gta aca agg ggg tcc gag cgc ttc cgg gac ctc gta ccc aac 240
167 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
168 65 70 75 80
170 tac aac ccc gac ata atc ttc aag gat gag gag aac agc ggc gca gac 288
171 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
172 85 90 95
174 cgc ctg atg aca gag cgt tgc aaa gaa cgg gtg aac gct cta gcc atc 336
175 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
176 100 105 110
178 gcg gtg atg aac atg tgg ccc gga gta cgc cta cgt gtg act gaa ggc 384
179 Ala Val Met Asn Met Trp Pro Glu Val Arg Leu Arg Val Thr Glu Gly
180 115 120 125
182 tgg gac gag gac ggc cac cac gca cag gat tca ctc cac tac gaa ggc 432
183 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
184 130 135 140
186 cgt gcc ttg gac atc acc acg tct gac cgt gac cgt aat aag tat ggt 480
187 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
188 145 150 155 160
190 ttg ttg gcg cgc cta gct gtg gaa gca gga ttc gac tgg gtc tac tac 528
191 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
192 165 170 175
194 gag tcc cgc aac cac atc cac gta tcc gtc aaa gct gat aac tca ctg 576
195 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
196 180 185 190

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236																	340	345	
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242	ctg	ctc	cct	qgg	qgt	gca	gtc	cag	ccg	act	ggc	atg	cat	tgg	tac	tct		1152	
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244																	370	375	
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267																	
269	20						25								30		
270	gtg	gtg	gqc	agc	cgc	cg	agg	ccg	cct	cgc	aag	ctc	gtg	cct	ctt	gcc	144
271	Val	Val	Gly	Ser	Arg	Arg	Arg	Pro	Pro	Arg	Lys	Leu	Val	Pro	Leu	Ala	
272																	
273	25						40									45	
274	tac	aag	cag	ttc	agc	ccc	aac	gtg	ccg	gag	aag	acc	ctg	gqc	gcc	agc	192
275	Tyr	Lys	Gln	Phe	Ser	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	Gly	Ala	Ser	
276																	
277	50						55									60	
278	ggg	cgc	tac	gaa	ggc	aag	atc	ycg	cgc	agc	tct	qag	cgc	ttc	aaa	gag	240
279	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu	
280																	
281	65						70									80	
282	ctc	acc	ccc	aac	tac	aat	ccc	gac	atc	atc	aag	gac	gag	gag	aac	288	
283	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	
284																	
285	85						90									95	
286	acg	gg	gcc	gac	cgc	ctc	atg	acc	cag	cgc	tgc	aag	gac	cgt	ctg	aac	336
287	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn	
288																	
289	100						105									110	
290	tca	ctg	gcc	atc	tct	gtc	atg	aac	cag	tgg	cct	gg	gtg	aaa	ctg	cgg	384
291	Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	
292																	
293	115						120									125	
294	gtg	acc	gaa	ggc	cgg	gat	qaa	gat	ggc	cat	cac	tca	gag	gag	tct	tta	432
295	Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	
296																	
297	130						135									140	
298	cac	tat	gag	ggc	cgc	gtg	gt	atc	acc	tca	gac	cgt	gac	cga	480		
299	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	
300																	
301	145						150									160	
302	aat	aag	tat	gga	ctg	ctg	gca	gg	gtg	gag	gcc	ggc	tcc	gac	528		
303	Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	
304																	
305	165						170									175	
306	tgg	gtg	tat	tac	gag	tcc	aag	gcc	cac	gt	tgc	tct	gtc	aag	tct	576	
307	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	
308																	
309	180						185									190	
310	gag	cat	tcc	gcc	gtc	gt	gat	gac	acc	tcc	ttt	cct	gcc	gg	gcc	624	
311	Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	
312																	
313	195						200									205	
314	cag	gtg	cgc	cta	gag	aac	ggg	gag	cg	gt	gcc	ctg	tca	gct	gt	aag	672
315	Gin	Val	Arg	Leu	Glu	Asn	Gly	Glu	Arg	Val	Ala	Leu	Ser	Ala	Val	Lys	
316																	
317	210						215									220	
318	cca	gga	gac	cg	gt	ctg	gcc	atg	ggg	gag	gt	gg	acc	ccc	acc	ttc	720
319	Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe	
320																	
321	225						230									240	
322	agt	gt	tg	ttt	att	ttc	ctg	gac	cg	g	cc	aac	cg	ctg	aga	gt	768
323	Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala	
324																	
325	245						250									255	
326	tcc	cag	gtc	atc	gag	act	cag	gt	cct	ccg	cgt	ogg	ctg	gca	ctc	acg	816
327	Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	
328																	
329	260						265									270	

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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/394,020B

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Input Set : A:\Huv3201.app
Output Set: N:\CRF3\11292000\I394020B.raw

L:734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1628 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
L:1628 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1628 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:2195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:2258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
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